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## RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/10/040,863

TIME: 08:51:13

Input Set : N:\Crf3\RULE60\10040863.raw

Output Set: N:\CRF3\02112002\J040863.raw

1 <110> APPLICANT: Eric H. Holmes et al.  
 2 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE  
 3 GM1-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES  
 4 THEREOF  
 5 <130> FILE REFERENCE: 8511-029  
 6 <140> CURRENT APPLICATION NUMBER: US/10/040,863  
 7 <141> CURRENT FILING DATE: 2001-11-01  
 8 <150> PRIOR APPLICATION NUMBER: US/09/298,886  
 9 <151> PRIOR FILING DATE: 1999-04-23  
 10 <160> NUMBER OF SEQ ID NOS: 29  
 11 <170> SOFTWARE: PatentIn Ver. 2.0  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 22  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Artificial Sequence  
 17 <220> FEATURE:  
 18 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 19 <400> SEQUENCE: 1  
 20 ggccgctttg ggaaccagat gg 22  
 22 <210> SEQ ID NO: 2  
 23 <211> LENGTH: 22  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 28 <400> SEQUENCE: 2  
 29 gggttacctg cgtgagcagc gc 22  
 31 <210> SEQ ID NO: 3  
 32 <211> LENGTH: 24  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Artificial Sequence  
 35 <220> FEATURE:  
 36 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 37 <400> SEQUENCE: 3  
 38 ttcccatcag aaggctcttc ctgc 24  
 40 <210> SEQ ID NO: 4  
 41 <211> LENGTH: 17  
 42 <212> TYPE: DNA  
 43 <213> ORGANISM: Artificial Sequence  
 44 <220> FEATURE:  
 45 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
 46 <400> SEQUENCE: 4  
 47 ccgcctccac catcttc 17

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Input Set : N:\Crif3\RULE60\10040863.raw

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49 <210> SEQ ID NO: 5
50 <211> LENGTH: 24
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
55 <400> SEQUENCE: 5
56   atgaattccc tccagcagcg aata                               24
58 <210> SEQ ID NO: 6
59 <211> LENGTH: 24
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
64 <400> SEQUENCE: 6
65   gccatggcca gcgcccaggt tcct                               24
67 <210> SEQ ID NO: 7
68 <211> LENGTH: 1149
69 <212> TYPE: DNA
70 <213> ORGANISM: Rattus norvegicus
71 <220> FEATURE:
72 <221> NAME/KEY: CDS
73 <222> LOCATION: (1)..(1143)
74 <400> SEQUENCE: 7
75   atg gcc agc gcc cag gtt cct ttc tcc ttt cct ctg gcc cac ttc ctc   48
76   Met Ala Ser Ala Gln Val Pro Phe Ser Phe Pro Leu Ala His Phe Leu
77     1             5             10             15
78   atc ttt gtc ttc gtg act tcc acc atc atc cac ctc cag cag cga ata   96
79   Ile Phe Val Phe Val Thr Ser Thr Ile His Leu Gln Gln Arg Ile
80             20             25             30
81   gtg aag ctc caa ccc ctg tca gag aag gaa tta ccg atg acg act caa   144
82   Val Lys Leu Gln Pro Leu Ser Glu Lys Glu Leu Pro Met Thr Thr Gln
83             35             40             45
84   atg tcc tcg gga aac aca gaa agc cca gag atg cga cgg gac agc gag   192
85   Met Ser Ser Gly Asn Thr Glu Ser Pro Glu Met Arg Arg Asp Ser Glu
86             50             55             60
87   cag cat ggg aat gga gag ctg cgg ggc atg ttc acg atc aat tcc att   240
88   Gln His Gly Asn Gly Glu Leu Arg Gly Met Phe Thr Ile Asn Ser Ile
89             65             70             75             80
90   ggc cgg ctg ggg aac cag atg ggc gaa tac gcc aca ctc ttt gca ctg   288
91   Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr Leu Phe Ala Leu
92             85             90             95
93   gcc agg atg aac gga cgg ctt gcg ttc atc ccc gca tcc atg cac aac   336
94   Ala Arg Met Asn Gly Arg Leu Ala Phe Ile Pro Ala Ser Met His Asn
95             100            105            110
96   gct cta gcg ccc atc ttc agg atc agc ctc ccg gtg tta cac agc gac   384
97   Ala Leu Ala Pro Ile Phe Arg Ile Ser Leu Pro Val Leu His Ser Asp
98             115            120            125
99   acg gcc aaa aag atc cca tgg cag aat tac cat ctc aac gac tgg atg   432

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Input Set : N:\Crf3\RULE60\10040863.raw

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100	Thr	Ala	Lys	Lys	Ile	Pro	Trp	Gln	Asn	Tyr	His	Leu	Asn	Asp	Trp	Met	
101		130					135					140					
102	gag	gag	cgt	tac	cgc	cac	att	ccg	gga	cac	ttt	gtg	cgc	ttc	acg	gga	480
103	Glu	Glu	Arg	Tyr	Arg	His	Ile	Pro	Gly	His	Phe	Val	Arg	Phe	Thr	Gly	
104		145				150					155					160	
105	tac	ccg	tgc	tcc	tgg	acc	ttc	tac	cac	cac	ctg	cgc	cca	gag	atc	ctg	528
106	Tyr	Pro	Cys	Ser	Trp	Thr	Phe	Tyr	His	His	Leu	Arg	Pro	Glu	Ile	Leu	
107					165					170					175		
108	aag	gag	ttc	acc	ctg	cat	gac	cac	gtg	cgg	gag	gag	gcc	cag	gcc	ttc	576
109	Lys	Glu	Phe	Thr	Leu	His	Asp	His	Val	Arg	Glu	Glu	Ala	Gln	Ala	Phe	
110				180					185					190			
111	ctg	cgt	ggt	ctg	cgg	gtg	aat	ggg	agc	cag	ccg	agt	act	ttt	gtg	ggt	624
112	Leu	Arg	Gly	Leu	Arg	Val	Asn	Gly	Ser	Gln	Pro	Ser	Thr	Phe	Val	Gly	
113			195					200					205				
114	gtc	cat	gtg	cgc	cga	ggg	gac	tat	gtg	cat	gtc	atg	cct	aat	gtg	tgg	672
115	Val	His	Val	Arg	Arg	Gly	Asp	Tyr	Val	His	Val	Met	Pro	Asn	Val	Trp	
116		210				215					220						
117	aag	ggc	gtg	gtg	gct	gac	cgg	ggt	tac	ctg	gaa	aag	gcc	ctg	gat	atg	720
118	Lys	Gly	Val	Val	Ala	Asp	Arg	Gly	Tyr	Leu	Glu	Lys	Ala	Leu	Asp	Met	
119		225				230					235					240	
120	ttc	cgg	gca	cgc	tat	tca	tct	cca	gtc	ttc	gtg	gtt	aca	agc	aac	ggt	768
121	Phe	Arg	Ala	Arg	Tyr	Ser	Ser	Pro	Val	Phe	Val	Val	Thr	Ser	Asn	Gly	
122				245						250				255			
123	atg	gcc	tgg	tgc	cgg	gag	aac	att	aat	gct	tcc	cga	gga	gac	gtg	gtg	816
124	Met	Ala	Trp	Cys	Arg	Glu	Asn	Ile	Asn	Ala	Ser	Arg	Gly	Asp	Val	Val	
125			260						265					270			
126	ttc	gcg	ggc	aat	ggt	att	gag	ggg	tcg	cca	gcc	aag	gac	ttc	gcg	ctg	864
127	Phe	Ala	Gly	Asn	Gly	Ile	Glu	Ser	Pro	Ala	Lys	Asp	Phe	Ala	Leu		
128		275						280					285				
129	ctc	acc	cag	tgc	aac	cac	acc	atc	atg	act	att	ggg	acc	ttt	ggg	att	912
130	Leu	Thr	Gln	Cys	Asn	His	Thr	Ile	Met	Thr	Ile	Gly	Thr	Phe	Gly	Ile	
131		290						295				300					
132	tgg	gct	gcc	tac	ctg	gca	ggt	ggt	gat	acc	atc	tac	tta	gcc	aac	tac	960
133	Trp	Ala	Ala	Tyr	Leu	Ala	Gly	Gly	Asp	Thr	Ile	Tyr	Leu	Ala	Asn	Tyr	
134		305				310					315					320	
135	acc	ctt	ccg	gat	tct	ccg	ttc	ctc	aaa	gtc	ttt	aag	cca	gag	gca	gcc	1008
136	Thr	Leu	Pro	Asp	Ser	Pro	Phe	Leu	Lys	Val	Phe	Lys	Pro	Glu	Ala	Ala	
137				325						330				335			
138	ttc	cta	ccc	gaa	tgg	gtg	ggc	atc	cct	gcc	gat	ctg	tcc	cca	ctc	ctt	1056
139	Phe	Leu	Pro	Glu	Trp	Val	Gly	Ile	Pro	Ala	Asp	Leu	Ser	Pro	Leu	Leu	
140			340						345					350			
141	aag	gca	tta	aca	cca	gcc	tgt	cct	cgg	tcc	cac	ttc	cac	ctc	aag	gca	1104
142	Lys	Ala	Leu	Thr	Pro	Ala	Cys	Pro	Arg	Ser	His	Phe	His	Leu	Lys	Ala	
143			355					360					365				
144	aaa	gga	gtc	act	tgt	tac	gtc	gca	gga	aga	gcc	ttc	tga	tgggaa			1149
145	Lys	Gly	Val	Thr	Cys	Tyr	Val	Ala	Gly	Arg	Ala	Phe					
146		370					375					380					
148	<210>	SEQ ID NO: 8															
149	<211>	LENGTH: 380															

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150 <212> TYPE: PRT
151 <213> ORGANISM: Rattus norvegicus
152 <400> SEQUENCE: 8
153 Met Ala Ser Ala Gln Val Pro Phe Ser Phe Pro Leu Ala His Phe Leu
154 1 5 10 15
155 Ile Phe Val Phe Val Thr Ser Thr Ile Ile His Leu Gln Gln Arg Ile
156 20 25 30
157 Val Lys Leu Gln Pro Leu Ser Glu Lys Glu Leu Pro Met Thr Thr Gln
158 35 40 45
159 Met Ser Ser Gly Asn Thr Glu Ser Pro Glu Met Arg Arg Asp Ser Glu
160 50 55 60
161 Gln His Gly Asn Gly Glu Leu Arg Gly Met Phe Thr Ile Asn Ser Ile
162 65 70 75 80
163 Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr Leu Phe Ala Leu
164 85 90 95
165 Ala Arg Met Asn Gly Arg Leu Ala Phe Ile Pro Ala Ser Met His Asn
166 100 105 110
167 Ala Leu Ala Pro Ile Phe Arg Ile Ser Leu Pro Val Leu His Ser Asp
168 115 120 125
169 Thr Ala Lys Lys Ile Pro Trp Gln Asn Tyr His Leu Asn Asp Trp Met
170 130 135 140
171 Glu Glu Arg Tyr Arg His Ile Pro Gly His Phe Val Arg Phe Thr Gly
172 145 150 155 160
173 Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu Arg Pro Glu Ile Leu
174 165 170 175
175 Lys Glu Phe Thr Leu His Asp His Val Arg Glu Glu Ala Gln Ala Phe
176 180 185 190
177 Leu Arg Gly Leu Arg Val Asn Gly Ser Gln Pro Ser Thr Phe Val Gly
178 195 200 205
179 Val His Val Arg Arg Gly Asp Tyr Val His Val Met Pro Asn Val Trp
180 210 215 220
181 Lys Gly Val Val Ala Asp Arg Gly Tyr Leu Glu Lys Ala Leu Asp Met
182 225 230 235 240
183 Phe Arg Ala Arg Tyr Ser Ser Pro Val Phe Val Val Thr Ser Asn Gly
184 245 250 255
185 Met Ala Trp Cys Arg Glu Asn Ile Asn Ala Ser Arg Gly Asp Val Val
186 260 265 270
187 Phe Ala Gly Asn Gly Ile Glu Gly Ser Pro Ala Lys Asp Phe Ala Leu
188 275 280 285
189 Leu Thr Gln Cys Asn His Thr Ile Met Thr Ile Gly Thr Phe Gly Ile
190 290 295 300
191 Trp Ala Ala Tyr Leu Ala Gly Gly Asp Thr Ile Tyr Leu Ala Asn Tyr
192 305 310 315 320
193 Thr Leu Pro Asp Ser Pro Phe Leu Lys Val Phe Lys Pro Glu Ala Ala
194 325 330 335
195 Phe Leu Pro Glu Trp Val Gly Ile Pro Ala Asp Leu Ser Pro Leu Leu
196 340 345 350
197 Lys Ala Leu Thr Pro Ala Cys Pro Arg Ser His Phe His Leu Lys Ala
198 355 360 365

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199      Lys Gly Val Thr Cys Tyr Val Ala Gly Arg Ala Phe
200          370                      375                      380
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203 <211> LENGTH: 1068
204 <212> TYPE: DNA
205 <213> ORGANISM: Rattus norvegicus
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (1)..(1062)
209 <400> SEQUENCE: 9
210      ctc cag cag cga ata gtg aag ctc caa ccc ctg tca gag aag gaa tta      48
211      Leu Gln Gln Arg Ile Val Lys Leu Gln Pro Leu Ser Glu Lys Glu Leu
212          1                      5                      10                      15
213      ccg atg acg act caa atg tcc tcg gga aac aca gaa agc cca gag atg      96
214      Pro Met Thr Thr Gln Met Ser Ser Gly Asn Thr Glu Ser Pro Glu Met
215          20                      25                      30
216      cga cgg gac agc gag cag cat ggg aat gga gag ctg cgg ggc atg ttc      144
217      Arg Arg Asp Ser Glu Gln His Gly Asn Gly Glu Leu Arg Gly Met Phe
218          35                      40                      45
219      acg atc aat tcc att ggc cgg ctg ggg aac cag atg ggc gaa tac gcc      192
220      Thr Ile Asn Ser Ile Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala
221          50                      55                      60
222      aca ctc ttt gca ctg gcc agg atg aac gga cgg ctt gcg ttc atc ccc      240
223      Thr Leu Phe Ala Leu Ala Arg Met Asn Gly Arg Leu Ala Phe Ile Pro
224          65                      70                      75                      80
225      gca tcc atg cac aac gct cta gcg ccc atc ttc agg atc agc ctc ccg      288
226      Ala Ser Met His Asn Ala Leu Ala Pro Ile Phe Arg Ile Ser Leu Pro
227          85                      90                      95
228      gtg tta cac agc gac acg gcc aaa aag atc cca tgg cag aat tac cat      336
229      Val Leu His Ser Asp Thr Ala Lys Lys Ile Pro Trp Gln Asn Tyr His
230          100                      105                      110
231      ctc aac gac tgg atg gag gag cgt tac cgc cac att ccg gga cac ttt      384
232      Leu Asn Asp Trp Met Glu Glu Arg Tyr Arg His Ile Pro Gly His Phe
233          115                      120                      125
234      gtg cgc ttc acg gga tac ccg tgc tcc tgg acc ttc tac cac cac ctg      432
235      Val Arg Phe Thr Gly Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu
236          130                      135                      140
237      cgc cca gag atc ctg aag gag ttc acc ctg cat gac cac gtg cgg gag      480
238      Arg Pro Glu Ile Leu Lys Glu Phe Thr Leu His Asp His Val Arg Glu
239          145                      150                      155                      160
240      gag gcc cag gcc ttc ctg cgt ggt ctg cgg gtg aat ggg agc cag ccg      528
241      Glu Ala Gln Ala Phe Leu Arg Gly Leu Arg Val Asn Gly Ser Gln Pro
242          165                      170                      175
243      agt act ttt gtg ggt gtc cat gtg cgc cga ggg gac tat gtg cat gtc      576
244      Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr Val His Val
245          180                      185                      190
246      atg cct aat gtg tgg aag ggc gtg gtg gct gac cgg ggt tac ctg gaa      624
247      Met Pro Asn Val Trp Lys Gly Val Val Ala Asp Arg Gly Tyr Leu Glu
248          195                      200                      205

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VERIFICATION SUMMARY

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